

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 18, 2001, 15:30:02 ; Search time 46.42 Seconds

(without alignments)  
745.007 Million cell updates/sec

Title: US-09-653-755A-4

Perfect score: 2427

Sequence: 1 EVQLQQSGPELVKPGASVMI.....RHEGLKNYTKTISRSPGK 454

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR68:\*  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### \*SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2190.5	90.3	474	1 G2MS11	Ig gamma-2b chain
2	2135	88.0	475	2 S01321	Ig gamma-2b chain
3	1835	75.6	469	2 S37483	Ig gamma-2a chain
4	1832.5	75.5	446	2 S40295	Ig gamma-2a chain
5	1797	74.0	405	1 G2MSBM	Ig gamma-2b chain
6	1439	59.3	444	2 PC4436	monoclonal antibod
7	1419	58.5	330	1 G2MSA	Ig gamma-2a chain
8	1414	58.3	399	1 G2MSAM	Ig gamma-2a chain
9	1385.5	57.1	335	1 G2MSAB	Ig gamma-2a chain
10	1326.5	54.7	333	2 PS0018	Ig gamma-2b chain
11	1321.5	54.4	472	2 S31459	Ig gamma-1 chain
12	1286.5	53.0	470	2 S22080	Ig heavy chain pre
13	1202.5	49.5	329	2 S00847	Ig gamma-2c chain
14	1170	48.2	329	1 G3MSC	Ig gamma-3 chain C
15	1159	47.8	398	1 G3MSM	Ig gamma-2a chain C
16	1150	47.4	324	1 G1MS	Ig gamma-1 chain C
17	1145	47.2	393	1 G1MSM	Ig gamma-1 chain C
18	1112	45.8	326	2 PS0017	Ig gamma-1 chain C
19	1100	45.3	330	2 PS0019	Ig gamma-1 chain C
20	1087	44.8	332	1 GHU	Ig gamma-1 chain C
21	1080.5	44.5	323	1 GHRB	Ig gamma-1 chain C
22	1080.5	44.5	329	1 G2GP	Ig gamma-2 chain C
23	1072.5	44.2	377	2 A60764	Ig gamma-3 chain C
24	1072.5	44.2	377	2 A23511	Ig gamma-3 chain C
25	1059	43.6	326	1 G2HU	Ig gamma-2 chain C
26	1058	43.4	327	2 I47159	Ig gamma-4 chain C
27	1054.5	43.2	328	2 I47160	Ig gamma-2b chain C
28	1049	43.2	328	2 I47161	Ig gamma-3 chain C
29	1028	42.4	328	2 I47161	Ig gamma-3 chain C

30	1023.5	42.2	308	2 C30554	Ig heavy chain C r
31	1022	42.1	328	2 I47158	Ig gamma 1 chain c
32	1014.5	41.8	246	2 S39050	Ig gamma chain - m
33	1008.5	41.6	348	2 S38864	Ig epsilon chain C
34	987.5	40.7	327	2 S06611	Ig gamma-2 chain C
35	918.5	37.8	374	2 S69339	Ig heavy chain V r
36	884	36.4	277	2 I47162	Ig gamma 4 chain c
37	855.5	35.2	231	2 PC4155	Ig gamma-2b chain c
38	819	33.7	549	2 S04845	Ig heavy chain pre
39	818.5	33.7	627	2 S14683	Ig mu chain precu
40	781.5	32.2	255	4 S31866	Ig gamma-1 chain C
41	778.5	32.1	221	2 S49220	Ig gamma-1 chain -
42	778	32.1	214	2 PC4202	monoclonal antibod
43	774.5	31.9	213	2 S68213	Ig heavy chain (Ma
44	774.5	31.9	234	2 PT0207	Ig gamma chain C r
45	771.5	31.8	289	1 G3H0W1	Ig gamma-3 heavy c

#### ALIGNMENTS

RESULT 1  
G2MS11  
Ig gamma-2b chain - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Mar-1980 #sequence\_revision 01-Dec-2000 #text\_change 01-Dec-2000  
C:Accession: S25057; A02157; A26235; A26232; A53598  
R:Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.  
submitted to the EMBL Data Library, July 1992  
A:Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific  
A:Reference number: S25057  
A:Accession: S25057  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-474 <FIS>  
R:Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Ometa, M.; Honjo, T.  
Nature 283, 786-789, 1980  
A:Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned fro  
A:Reference number: A02157; MUID:80120716  
A:Contents: a allele  
A:Accession: A02157  
A:Molecule type: DNA  
A:Residues: 138-161, 'L', 163-189, 'FP', 193-474 <YAM>  
A:Cross-references: GB:J00461  
A:Note: the sequence was determined from the germline gene  
R:Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.  
Science 206, 1299-1303, 1979  
A:Title: Structure of the constant and 3' untranslated regions of the murine gamma2b  
A:Reference number: A26235; MUID:80081501  
A:Contents: MPC 11  
A:Accession: A26235  
A:Molecule type: mRNA  
A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TUI>  
A:Note: Lys-474 is probably removed posttranslationally  
R:Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.  
Science 206, 1303-1306, 1979  
A:Title: Sequence of the cloned gene for the constant region of murine gamma2b immuno  
A:Reference number: A26232; MUID:80081502  
A:Accession: A26232  
A:Molecule type: DNA  
A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TUI>  
R:Ollo, R.; Rougeon, F.  
Nature 296, 761-763, 1982  
A:Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and g  
A:Reference number: A26233; MUID:82173203  
A:Contents: b allele  
A:Accession: A26233  
A:Molecule type: DNA  
A:Residues: 138-161, 'L', 163-189, 'FP', 193-300, 'R', 302-331, 'A', 333-437, 'DI', 440-474 <OL  
A:Cross-references: GB:J00461  
R:Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takah  
J. Biol. Chem. 269, 12345-12350, 1994

A>Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.  
A:Reference number: A53598; MUID:94216359  
A:Accession: A53598  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 234-251 <KIM>  
C:Comment: The a allele sequence is shown.  
C:Genetics:  
A:Introns: 138/1; 236/1; 258/1; 368/1  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a C:Superfamily: Immunoglobulin C region; Immunoglobulin homology  
C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin  
F:157-222/Domain: immunoglobulin homology <IM1>  
F:236-257/Region: hinge  
F:281-350/Domain: immunoglobulin homology <IM2>  
F:387-454/Domain: immunoglobulin homology <IM3>  
F:152/Disulfide bonds: Interchain (to light chain) #status predicted  
F:164-220,288-348,394-452/Disulfide bonds: #status predicted  
F:247,250,253,256/Disulfide bonds: Interchain (to heavy chain) #status predicted  
F:324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 90.3%; Score 2190.5; DB 1; Length 474;  
Best Local Similarity 91.2%; Pred. No. 1.4e-123;  
Matches 415; Conservative 10; Mismatches 29; Indels 1; Gaps 1;

QY 1 EVOLQSGPELVKPGASWISCRTSAFTENTVHMVKOSHGESLEWIGINPYGGSIF 60  
DB 20 EVOLQSGPELVKPGASWISCRTSAFTENTVHMVKOSHGESLEWIGINPYGGSIF 79  
QY 61 SPKFKGKATLVYDKSSSTAYMELSLTSDSAVYCARAGAYFDYWGQGLTVTSAAK 120  
DB 80 NEFKGKATLVYDKSSSTAYMELSLTSDSAVYCARAGAYFDYWGQGLTVTSAAK 139  
QY 121 TRPPSYVPLAPGCGDTGSSVTLGCLVKGYPESVTVTNMNSGLSSVHTF-PALLQSG 179  
DB 140 TRPPSYVPLAPGCGDTGSSVTLGCLVKGYPESVTVTNMNSGLSSVHTF-PALLQSG 199  
QY 180 YTMSSSVTPSSVTPSQVTCVSAHPASTVYDKKLEPSPGISTINPCPKCKCHCPA 239  
DB 200 YTMSSSVTPSSVTPSQVTCVSAHPASTVYDKKLEPSPGISTINPCPKCKCHCPA 259  
QY 240 NEEGGSVFIFPPNIKDVLMISLTPKVTGVVVDSEDDPVOISFVNNVEVHTAQTQT 299  
DB 260 NEEGGSVFIFPPNIKDVLMISLTPKVTGVVVDSEDDPVOISFVNNVEVHTAQTQT 319  
QY 300 REDYNTITRVVSTLPIQHODMMSGKEFKCKVNNKDLPSPIERTISKIGLVAPQVYILP 359  
DB 320 REDYNTITRVVSTLPIQHODMMSGKEFKCKVNNKDLPSPIERTISKIGLVAPQVYILP 379  
QY 360 PRAEQLSRKDVSLTCLVGFNPGDISVEMTNGHTEENKDTAPVLDSDGSYFYISKLN 419  
DB 380 PRAEQLSRKDVSLTCLVGFNPGDISVEMTNGHTEENKDTAPVLDSDGSYFYISKLN 439  
QY 420 KTSKWEKTDSCNVNHEGLKNYLLKKTISRSPGK 454  
DB 440 KTSKWEKTDSCNVNHEGLKNYLLKKTISRSPGK 474

RESULT 2  
S01321  
Ig gamma-2b chain precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 23-Jul-1999  
C:Accession: S01321

R:de Waale, P.; Feys, V.; van de Voorde, A.; Molmans, F.; Fiers, W.  
Eur. J. Biochem. 176, 287-295, 1988  
A>Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed at  
A:Reference number: S01320; MUID:88329081  
A:Accession: S01321  
A:Molecule type: mRNA  
A:Residues: 1-475 <DEI>

A:Cross-references: EMBL:X13188; NID:g51780; PIDN:CAA31580.1; PID:g51781  
A>Note: this sequence was determined from the differentiated gene  
C:Superfamily: Immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-475/Product: Ig gamma-2b chain #status predicted <MAT>  
F:159-223/Domain: immunoglobulin homology <IMX>

Query Match 88.0%; Score 2135; DB 2; Length 475;  
Best Local Similarity 88.4%; Pred. No. 3e-120;  
Matches 403; Conservative 15; Mismatches 36; Indels 2; Gaps 1;

QY 1 EVOLQSGPELVKPGASWISCRTSAFTENTVHMVKOSHGESLEWIGINPYGGSIF 60  
DB 20 EVOLQSGPELVKPGASWISCRTSAFTENTVHMVKOSHGESLEWIGINPYGGSIF 79  
QY 61 SPKFKGKATLVYDKSSSTAYMELSLTSDSAVYCARAGAYFDYWGQGLTVTSAAK 118  
DB 80 NEFKGKATLVYDKSSSTAYMELSLTSDSAVYCARAGAYFDYWGQGLTVTSAAK 139  
QY 119 AKTTPSYVPLAPGCGDTGSSVTLGCLVKGYPESVTVTNMNSGLSSVHTFPALLQSG 178  
DB 140 AKTTPSYVPLAPGCGDTGSSVTLGCLVKGYPESVTVTNMNSGLSSVHTFPALLQSG 199  
QY 179 LYTMSSSVTPSSVTPSQVTCVSAHPASTVYDKKLEPSPGISTINPCPKCKCHCPA 238  
DB 200 LYTMSSSVTPSSVTPSQVTCVSAHPASTVYDKKLEPSPGISTINPCPKCKCHCPA 259  
QY 239 PNEGGPSVFIFPPNIKDVLMISLTPKVTGVVVDSEDDPVOISFVNNVEVHTAQTQT 298  
DB 260 PNEGGPSVFIFPPNIKDVLMISLTPKVTGVVVDSEDDPVOISFVNNVEVHTAQTQT 319  
QY 299 HREDYNTITRVVSTLPIQHODMMSGKEFKCKVNNKDLPSPIERTISKIGLVAPQVYIL 358  
DB 320 HREDYNTITRVVSTLPIQHODMMSGKEFKCKVNNKDLPSPIERTISKIGLVAPQVYIL 379  
QY 359 PRAEQLSRKDVSLTCLVGFNPGDISVEMTNGHTEENKDTAPVLDSDGSYFYISKLN 418  
DB 380 PRAEQLSRKDVSLTCLVGFNPGDISVEMTNGHTEENKDTAPVLDSDGSYFYISKLN 439  
QY 419 KTSKWEKTDSCNVNHEGLKNYLLKKTISRSPGK 454  
DB 440 KTSKWEKTDSCNVNHEGLKNYLLKKTISRSPGK 475

RESULT 3  
S37483

Ig gamma-2a chain - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S37483  
R:Ducancel, F.F.D.  
submitted to the EMBL Data Library, February 1993  
A:Reference number: S37483  
A:Accession: S37483  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-469 <DUC>  
A:Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253  
C:Superfamily: Immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:276-345/Domain: immunoglobulin homology <IMX>

Query Match 75.6%; Score 1835; DB 2; Length 469;  
Best Local Similarity 75.7%; Pred. No. 2.2e-102;  
Matches 345; Conservative 44; Mismatches 59; Indels 8; Gaps 3;

QY 1 EVOLQSGPELVKPGASWISCRTSAFTENTVHMVKOSHGESLEWIGINPYGGSIF 60  
DB 20 EVOLQSGPELVKPGASWISCRTSAFTENTVHMVKOSHGESLEWIGINPYGGSIF 79



QY	119	AKTTPPSVYPLAPGGDITGSSVTIGCLVKGYPSPSYTNWNSGSLSSVHFPPLLQSG	178
Dp	1	AKTTPPSVYPLAPGGDITGSSVTIGCLVKGYPSPSYTNWNSGSLSSVHFPPLLQSG	60
QY	179	LYTMSSSVTVBPSSIMPSTQVTCVSAHPASSITTVDKKLEBSGFISTITNCPQPECKHCQPA	238
Dp	61	LYTMSSSVTVBPSSIMPSTQVTCVSAHPASSITTVDKKLEBSGFISTITNCPQPECKHCQPA	120
QY	239	PNLEGGPSVFIFPPPIKQVLMISLTPKVTQVYVDVSEDDPDVQISMFVNNVSVHTAQAOT	298
Dp	121	PNLEGGPSVFIFPPPIKQVLMISLTPKVTQVYVDVSEDDPDVQISMFVNNVSVHTAQAOT	180
QY	299	HREDYNSTIRVYVSTLPIDQHDMMSGEKCKAYNNKDLPSPIERTTSKIKGLVRAQVYIL	358
Dp	181	HREDYNSTIRVYVSTLPIDQHDMMSGEKCKAYNNKDLPSPIERTTSKIKGLVRAQVYIL	240
QY	359	PPPAOLSRKDVLSLCLVYVGFNPQDISVEWTSNGHTHEENYKQTAVALDSDGSYFYISKLN	418
Dp	241	PPPAOLSRKDVLSLCLVYVGFNPQDISVEWTSNGHTHEENYKQTAVALDSDGSYFYISKLN	300
QY	419	MKTSMEKTDSPSCVNRHDEGLKNYLLKKTISRSPG	453
Dp	301	MKTSMEKTDSPSCVNRHDEGLKNYLLKKTISRSPG	335

RESULT 6  
PC4436  
monoclonal antibody 13-1 heavy chain - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 04-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 21-Jan-2000  
C:Accession: PC4436  
R:Atsuh, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.  
Biochem. Biophys. Res. Commun. 240, 566-572, 1997  
A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyry  
A:Reference number: JCS810; MUID:98063277  
A:Accession: PC4436  
A:Molecule type: protein  
A:Residues: 1-444 <AKRA>  
C:Comment: This catalytic antibody has peroxidase oxidase activity. It is directed against  
C:Superfamily: Immunoglobulin C region; Immunoglobulin homology  
F:251-320/Domains: Immunoglobulin homology <IMM>  
F:22/Disulfide bonds: Interchain (to 98) #status predicted  
F:99/Disulfide bonds: Interchain (to 109) #status predicted

	Query March 59.3%:	Score 1439:	DB 2:	Length 444:
	Best Local Similarity 59.3%:	Pred. No. 8.5e-79:		
	Matches 271:	Conservative 68:	Mismatches 102:	Indels 16:
			Gaps 6:	
QY	1	EVOLQSGPELVKPGASVAMISCRTSAYTFTENTVYMWQSHGESLEWJGCI---NPPYGG	57	
		:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :		
Db	1	EVQXVNTGCGGLVRGNSLKLKSLCTISGFTFSNVBMHMLQPPGKRLKLEMLAVITYVSDNNGA	60	
QY	58	SIFSEKFEKGKATLVYDKSSSTAYMELRSLTSDSAVYYICARRAGAYYYDYGQGTTLTVS	117	
		:: :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :		
Db	61	K-YAESVGRFTTISKDDKSSVYLQMNRLREDDATYYCCRTPMWYADCMGQGSVTVS	119	
QY	118	SAKTTTPPVYPLAPGCGDGTSSVTLGCLVKGYPESTVYMWNSGSLSSVHTPALLOS	177	
		:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :		
Db	120	SAKTTTPPVYPLAPGSAQOTNSMTLGLCVKGYRPEPVYVWNSGSLSSGVHTFPAAVLQS	179	
QY	178	GLYTMSSSVTPSSSTWPSQVTCGSAVHPASSTVDKLEPBGPISTINPCPCRECHKCP	237	
		:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :		
Db	180	DLYTLSSSVTPSSSTWPSPEYVTCNVNHPASSTYKDKITVP-----RDC-GCKPC-ICT	230	
QY	238	APNLEGGPSVTLFPNNIKDVTLMISLTPEKVTGVVVDVSEDDPDVOISMFVNNVEVHTAQO	297	
		:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :		
Db	231	VPEVS---SVETFPKPKPDVLTILTPKVTGVVVDISKDDEVOFQSWFVDVEVHTAQO	287	
QY	298	THRDYNTSTIVVSTLPIHOHODMMSGKFEKCKVNNKDLPSPIETPISIKIKLVAPQVYI	357	
		:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :		
Db	288	PREQGFNSTRSVSELPMDHODMLNGKEKCKRVNSAAPAIETKTIISTKCRPAPQVYT	347	

[illegible]

RESULT	7
G2MSA	

Ig gamma-2a chain C region, secreted form (allele a) - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Sep-1960 #sequence\_revision 01-Sep-1981 #text\_change 16-Jun-2000  
 C:Accession: A02152; A32657; A32658  
 R:Stokrov, J.L.; Aultrey, C.; Rougeon, F.  
 Nucleic Acids Res. 8, 3143-3155, 1980  
 A:Title: Structure of the constant and 3' untranslated regions of the murine Balb/c  
 A:Reference number: A02152; MUID:81076554  
 A:Accession: A02152  
 A:Molecule type: mRNA  
 A:Residues: 1-330 <STK>  
 A:Cross-references: GB:V00798; NID:951835; PIDN:CAA24178.1; PID:91333984  
 R:Yamawaki-Kataoka, Y.; Miyata, T.; Honjo, T.  
 Nucleic Acids Res. 9, 1365-1381, 1981  
 A:Title: The complete nucleotide sequence of mouse immunoglobulin gamma 2 A gene and  
 A:Reference number: A32657; MUID:81198976  
 A:Accession: A32657  
 A:Molecule type: DNA  
 A:Residues: 1-330 <YAM>  
 A:Cross-references: GB:J00470  
 A:Note: the sequence was determined from the germ-line gene  
 R:Ollio, R.; Aultrey, C.; Morchamps, C.; Rougeon, F.  
 Proc. Natl. Acad. Sci. U.S.A. 78, 2442-2446, 1981  
 A:Title: Comparison of mouse immunoglobulin gamma-2A and gamma-2B chain genes suggest  
 A:Reference number: A32658; MUID:81223894  
 A:Accession: A32658  
 A:Molecule type: DNA  
 A:Residues: 1-330 <OLL>  
 A:Note: the sequence was determined from the germ-line gene  
 A:Note: Lys-330 is removed posttranslationally  
 R:Bourgois, A.; Fougereau, M.; Rocca-Serra, J.  
 Eur. J. Biochem. 43, 423-435, 1974  
 A:Title: Determination of the primary structure of a mouse IgG2a immunoglobulin: amln  
 A:Reference number: A32659; MUID:74175517  
 A:Contents: annotation; myeloma protein MOPC 173  
 A:Note: this is one paper in a series reporting the sequence; for additional reference  
 A:Note: this sequence differs from that shown at a number of positions  
 R:de Preval, C.; Fougereau, M.  
 Eur. J. Biochem. 30, 452-462, 1972  
 A:Title: Determination of the primary structure of a mouse gammaG2a immunoglobulin. I  
 A:Reference number: A32660; MUID:73056887  
 A:Contents: annotation; MOPC 173, disulfide bonds  
 C:Genetics:  
 A:Introns: 1/1; 98/1, 114/1, 224/1  
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (C  
 C:ain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunogl  
 F:20-84/Domain: immunoglobulin homology <IM1>  
 F:98-113/Region: hinge  
 F:137-206/Domain: immunoglobulin homology <IM2>  
 F:243-310/Domain: immunoglobulin homology <IM3>  
 F:15/Disulfide bonds: interchain (to light chain) #status experimental  
 F:27-82,144-204,250-308/Disulfide bonds: #status experimental  
 F:107,110,112/Disulfide bonds: interchain (to heavy chain) #status experimental  
 F:180/Binding site: carbohydrate (Asn) (covalent) #status predicted















